On page 5, the paragraph at lines 3 and 4 has been replaced with the following:

Figure 3 represents a comparison of the amino acid sequence between the human (SEQ ID NO: 3) and the porcine (SEQ ID NO: 4) MC4R gene.

On page 5, the paragraph at lines 6-8 has been replaced with the following:

Figure 5 depicts an alignment of partial nucleotide and amino acid sequences of two different porcine MC4R alleles. As can be seen, the partial nucleotide sequence of allele 1 (SEQ ID NO: 27) differs from that of allele 2 (SEQ ID NO: 28) by virtue of a guanine→adenine substitution. This substitution results in a corresponding amino acid change (indicated by arrow) from aspartic acid (D) in the partial amino acid sequence of allele 1 (SEQ ID NO: 29) to asparagine (N) in allele 2 (SEQ ID NO: 30).

On page 5, the paragraph at lines 11-18 has been replaced with the following:

Figure 7 depicts multiple-alignments of the putative seventh transmembrane domain of porcine MC4R with other MCRs and GPCRs. The "*" represents the predicted sequence positions for porcine MC4R ("pMC4R") (SEQ ID NO: 11). The other amino acid sequences ("hMC4R"; "rMC4R"; "sheep MC5R"; "bovine MC5R"; "bovine MC2R"; "hMC3R"; "mMC3R"; "hMC2R"; "hMC1R"; "bEDG-2R"; "hEDG-4R"; "human cannab"; "hH2AB"; "rSSR2"; "hGAL-R") were obtained from the GenBank database (respectively, accession numbers P32245 (SEQ ID NO:12), P70596 (SEQ ID NO:13), P41983 (SEQ ID NO:14), P56451 (SEQ ID NO:15), P34974 (SEQ ID NO:16), P41968 (SEQ ID NO:17), P33033 (SEQ ID NO:18), Q01718 (SEQ ID NO:19), Q01726 (SEQ ID NO:20), Q28031 (SEQ ID NO:21), AF011466 (SEQ ID NO:22), P21554 (SEQ ID NO:23), P18089 (SEQ ID NO:24), P30680 (SEQ ID NO:25), P47211 (SEQ ID NO:26)). The missense variant in porcine MC4R substituted amino acid N for D in the position marked with an arrow. The Asp (D) residue is highly conserved among MCRs, and the Asn (N) residue is well conserved in most other GPCRs.

On page 6, the paragraph at lines 23-29 has been replaced with the following:

Another embodiment of the invention provides a kit for assaying the presence in a MC4R gene sequence of a genetic marker. The marker being indicative of inheritable traits of fat

content, growth rate, and/or feed consumption. The kit in a preferred embodiment also includes novel PCR primers comprising 4-30 contiguous bases on either side of the polymorphism to provide an amplification system allowing for detection of the *Taq I* polymorphism by PCR and *Taq I* digestion of PCR products. The preferred primers are SEQ ID NO: 7 and SEQ ID NO: 8.

On page 7, the paragraph at lines 21-30 has been replaced with the following:

From sequence data, it was observed that in allele 2 the guanine is substituted with an adenine at position 678 of the PCR product or at position 298 amino acid of the MC4R protein changing the aspartic acid codon (GAU) into an asparagine codon (AAU). The PCR test for the polymorphism used a forward primer of 5'-TGG CAA TAG CCA AGA ACA AG-3' (SEQ. ID NO: 5) and a reverse primer of 5'-CAG GGG ATA GCA ACA GAT GA-3' (SEQ. ID NO: 6). Pig specific primers used were a forward primer of 5'-TTA AGT GGA GGA AGA AGG-3' (SEQ. ID NO: 7) and a reverse primer of 5'-CAT TAT GAC AGT TAA GCG G-3' (SEQ ID NO: 8). The resulting amplified product of about 750 bp, when digested with *Taq I*, results in allelic fragments of 466, 225, and 76 bp (allele 1) or 542 and 225 bp (allele 2).

On page 8, the paragraph at lines 8-25 has been replaced with the following:

Other possible techniques include non-gel systems such as TAQMAN™ (Perkin Elmer). In this system, oligonucleotide PCR primers are designed that flank the mutation in question and allow PCR amplification of the region. A third oligonucleotide probe is then designed to hybridize to the region containing the base subject to change between different alleles of the gene. This probe is labeled with fluorescent dyes at both the 5' and 3' ends. These dyes are chosen such that while in this proximity to each other the fluorescence of one of them is quenched by the other and cannot be detected. Extension by *Taq* DNA polymerase from the PCR primer positioned 5' on the template relative to the probe leads to the cleavage of the dye attached to the 5' end of the annealed probe through the 5' nuclease activity of the *Taq* DNA polymerase. This removes the quenching effect allowing detection of the fluorescence from the dye at the 3' end of the probe. The discrimination between different DNA sequences arises through the fact that if the hybridization of the probe to the template molecule is not complete, i.e., there is a mismatch of some form, the cleavage of the dye does not take place. Thus, only if